

ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-931-858E-199

Query Match 61.8%; Score 291; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 7e-53;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 181 GCCTGTCTGCTGCATGCCAGCTGTGGAGCTGTGAGCTGTCCCTGGCAGAGTAGGCGCTG 240
Db 1 GCCTGTCTGCTGCATGCCAGCTGTGGAGCTGTGAGCTGTCCCTGGCAGAGTAGGCGCTG 60
QY 241 GGCTAGCCCTCAGAGGAGAAGGTGTCATCTTCCGCTACTGCGCGCGCAGCTGCCCGCTGGT 300
Db 61 GGCTAGCCCTCAGAGGAGAAGGTGTCATCTTCCGCTACTGCGCGCGCAGCTGCCCGCTGGT 120
QY 301 GCCCGACCCAGCATGCCCTGGCGCTGGCGCGCTGCGCGCTGCGCGCGCAGGCGCCAGCGT 360
Db 121 GCCCGACCCAGCATGCCCTGGCGCTGGCGCGCTGCGCGCTGCGCGCGCAGGCGCCAGCGT 180
QY 361 GGCGCTGTGCTGCCGCGCCACTCGCTACACGAGCTGGCGCTTCCCTGATGACCGCCACCGC 420
Db 181 GGCGCTGTGCTGCCGCGCCACTCGCTACACGAGCTGGCGCTTCCCTGATGACCGCCACCGC 240
QY 421 TGGCAGCGGCTGCCCGAGCTCTCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTGA 471
Db 241 TGGCAGCGGCTGCCCGAGCTCTCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTGA 291

RESULT 6

US-08-931-858E-200/c
Sequence 200, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS

STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-931-858E-200

Query Match 61.8%; Score 291; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 7e-53;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 181 GCCTGTCTGCTGCATGCCAGCTGTGGAGCTGTGAGCTGTCCCTGGCAGAGTAGGCGCTG 240
Db 291 GCCTGTCTGCTGCATGCCAGCTGTGGAGCTGTGAGCTGTCCCTGGCAGAGTAGGCGCTG 232
QY 241 GGCTAGCCCTCAGAGGAGAAGGTGTCATCTTCCGCTACTGCGCGCGCAGCTGCCCGCTGGT 300
Db 231 GGCTAGCCCTCAGAGGAGAAGGTGTCATCTTCCGCTACTGCGCGCGCAGCTGCCCGCTGGT 172
QY 301 GCCCGACCCAGCATGCCCTGGCGCTGGCGCGCTGCGCGCTGCGCGCGCAGGCGCCAGCGT 360
Db 171 GCCCGACCCAGCATGCCCTGGCGCTGGCGCGCTGCGCGCTGCGCGCGCAGGCGCCAGCGT 112
QY 361 GGCGCTGTGCTGCCGCGCCACTCGCTACACGAGCTGGCGCTTCCCTGATGACCGCCACCGC 420
Db 111 GGCGCTGTGCTGCCGCGCCACTCGCTACACGAGCTGGCGCTTCCCTGATGACCGCCACCGC 52
QY 421 TGGCAGCGGCTGCCCGAGCTCTCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTGA 471
Db 51 TGGCAGCGGCTGCCCGAGCTCTCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCTGA 1

RESULT 7

US-08-931-858E-201
Sequence 201, Application US/08931858E
Patent No. 6222022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-931-858E-201

Query Match 61.4%; Score 289.4; DB 4; Length 291;
Best Local Similarity 99.7%; Pred. No. 1.5e-52;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 GCCCTGCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGCGTGCGCAGAGTAGGCCGTG 240
Db 1 GCCCTGCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGCGTGCGCAGAGTAGGCCGTG 60

QY 241 GGCTAGCCCTCAGAGGAGAGGTTCATCTTCCGCTACTGCGCGGCGAGCTGCCCGCTGTG 300
Db 61 GGCTAGCCCTCAGAGGAGAGGTTCATCTTCCGCTACTGCGCGGCGAGCTGCCCGCTGTG 120

QY 301 GCCCGACCCAGATGGCTGGCGCTGGCGCTGCGCGGCTGCGAGGGCCGAGGCCACAGGT 360
Db 121 GCCCGACCCAGATGGCTGGCGCTGGCGCTGCGCGGCTGCGAGGGCCGAGGCCACAGGT 180

QY 361 GGGCCCTGCTGCGGCGCCACTCGCTACACCGAGCTGGCGCTGCGCGCTGCGCGCTGCG 420
Db 181 GGGCCCTGCTGCGGCGCCACTCGCTACACCGAGCTGGCGCTGCGCGCTGCGCGCTGCG 240

QY 421 TGGCAGCGCTGCCCGAGCTCTCGCGGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 471
Db 241 TGGCAGCGCTGCCCGAGCTCTCGCGGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 291

RESULT 8
US-08-931-858E-202/c
Sequence 202, Application US/08931858E
Patent No. 622022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-931-858E-202

Query Match 61.4%; Score 289.4; DB 4; Length 291;
Best Local Similarity 99.7%; Pred. No. 1.5e-52;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 GCCCTGCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGCGTGCGCAGAGTAGGCCGTG 240
Db 291 GCCCTGCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGCGTGCGCAGAGTAGGCCGTG 232

QY 241 GGCTAGCCCTCAGAGGAGAGGTTCATCTTCCGCTACTGCGCGGCGAGCTGCCCGCTGTG 300
Db 231 GGCTAGCCCTCAGAGGAGAGGTTCATCTTCCGCTACTGCGCGGCGAGCTGCCCGCTGTG 172

QY 301 GCCCGACCCAGATGGCTGGCGCTGGCGCTGCGCGGCTGCGAGGGCCGAGGCCACAGGT 360
Db 171 GCCCGACCCAGATGGCTGGCGCTGGCGCTGCGCGGCTGCGAGGGCCGAGGCCACAGGT 112

QY 361 GGGCCCTGCTGCGGCGCCACTCGCTACACCGAGCTGGCGCTGCGCGCTGCGCGCTGCG 420
Db 111 GGGCCCTGCTGCGGCGCCACTCGCTACACCGAGCTGGCGCTGCGCGCTGCGCGCTGCG 471

QY 421 TGGCAGCGCTGCCCGAGCTCTCGCGGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 471
Db 51 TGGCAGCGCTGCCCGAGCTCTCGCGGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCG 1

RESULT 9
US-08-931-858E-222
Sequence 222, Application US/08931858E
Patent No. 622022
GENERAL INFORMATION:
APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY D
APPLICANT: KOTZBAUER, PAUL T
APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, ROBERT
APPLICANT: DESAUVAGE, FRED
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:


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: Sequence 191, Application US/08931858E
: Patent No. 622022
: GENERAL INFORMATION:
: APPLICANT: JOHNSON, EUGENE M
: APPLICANT: MILBRANDT, JEFFREY D
: APPLICANT: KOTZBAUER, PAUL T
: APPLICANT: LAMPE, PATRICIA A
: APPLICANT: KLEIN, ROBERT
: APPLICANT: DESAUVAGE, PRED
: TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
: NUMBER OF SEQUENCES: 239
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HOWELL & HAFERKAMP, L.C.
: STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
: CITY: ST. LOUIS
: STATE: MO
: COUNTRY: USA
: ZIP: 63105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/931.858E
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: HOLLAND, DONALD R.
: REGISTRATION NUMBER: 35,197
: REFERENCE/DOCKET NUMBER: 971486
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 314-727-5188
: TELEFAX: 314-727-6092
: INFORMATION FOR SEQ ID NO: 191:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 471 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: PS-08-931-858E-191

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	Matches	348;	Conservative	0;	Mismatches	120;	Indels	6;
	Gaps	2;						
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DG								
DG	411	GGCTGGGTCTTGTATCTTAAGAGGCTCTCGGGCAGAT---	355					
QY	121	GTGGCAAAAGGCTGAGGAGACCTGTGCTGGCACCCACC--CCGCCCTTGCCGCTGCGC	177					
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QY	354	ATGCGACAGACTGAAGGACCTGGAAGCCCCATCAGGGTAACAACATGTCCGCCATTCCA	295					
QY	178	CGAGCCCTGTGTGTTCATCCAGCTGTGGAGCCTGACCCCTGTCGGTGGCAGAGACTAGGC	237					
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DG	294	AGAGCCTTACCTGTTTGTGGCGCTGTGGAGCCTGACCTACCAAGTGGCTGAGCTTGGC	235					
QY	238	CTGGGCTACGCTCAGAGGAGAGGTCATCTTCGGCTACTGGCGGGCAGAGTGCCTCGT	297					
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DG	234	CTGGGCTATGCTCTCAGAGGAGAAGATTATCTTCGATACTGTGTGGCAGCTGTCCCCAA	175					
QY	298	GGTCCCCGACCCAGCATGGCTTCGGCTGGCCGGCTGACGGCCAGGCGGAGCCAC	357					
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DG	174	GAGTTCGTATCCCAAGCAGATCTGGTGTGGCCGCTCTTCGAGGCGAAGGTCGAGCTCAT	115					
QY	358	GGTGGGCGCTCTGCGCGGCCACCTCGCTACACCGACAGTGGCTTCTCGATGACCGCCAC	417					

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Db 114 GCAGACCTTGCTGCGACGCCACGAGTGTGCTGTGACCTTGCTGATGACGACCCAC 5
QY 418 CGCTGCGACGCGCTGCCACGACTCTCGCGCGGCTCGCTCGCGGCTGTGCTGGCTGA 471
Db 54 CATGCGACGAGCTGCCTCAGCTCTCAGCCCGCAGCTGTGCGCTGTGCTGGCTGA 1

RESULT 14
US-08-981-739-175
: Sequence 175, Application US/08981739
: Patent No. 6232449
: GENERAL INFORMATION:
: APPLICANT: JOHNSON JR., EUGENE M.
: MILBRANDT, JEFFREY D.
: KOTZBAUER, PAUL T.
: LAMPE, PATRICIA A.
: TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
: NUMBER OF SEQUENCES: 176
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HOWELL & HAFERKAMP, L.C.
: STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
: CITY: ST. LOUIS
: STATE: MISSOURI
: COUNTRY: US
: ZIP: 63105-1817
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/981.739
: FILING DATE: 31-Aug-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US97/03461
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: HOLLAND, DONALD R.
: REGISTRATION NUMBER: 35,197
: REFERENCE/DOCKET NUMBER: 976163
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314) 727-5188
: TELEFAX: (314) 727-6092
: INFORMATION FOR SEQ ID NO: 175:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 405 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 175:
US-08-981-739-175

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	Query Match	44.1%	Score	207.6;	DB 4;	Length	405;		
	Best Local Similarity	79.4%	Pred. No.	1.9e-35;					
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Db	156	AGTGGCTGAGCTGGSCCTGGGCTATGCTCCGAGAGAGAAGGTCACTTCCCATACTGTGC	215						
Qy	282	CGGCAGCTGCCCCCGTGTGCTGCCGACCCACAGATGGCCTGGCGTGGCCCCGGCTGCAGGG	341						
Db	216	TGGCAGCTGTCCCNAAGAGGCCGTATCCACGACAGTCTGGTACTGGCCCCGGCTTCGAGG	275						
Qy	342	CCAGGGCCGAGCCCCACGCTGGGGCCCTGCTGCCGGCCCCACTCGCTACACCGAGCTGGGCCATT	401						
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:32:18 ; Search time 313 Seconds
(without alignments)
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Title: US-09-220-617b-203

Perfect score: 471

Sequence: 1 ATGGCGGTAGGAGACTCT.....CCTGGGCTGTGGTGGCTGA 471

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471	100.0	471	20	AA60507 Human pre-pro pers
2	467.8	99.3	471	20	AA60509 WO9914235 Seq ID N
3	376	79.8	556	21	AAZ50334 Human Persephin-AR
4	376	79.8	556	21	AAZ50337 Human Persephin-AR
5	343.4	72.9	974	24	ABQ54526 Human ovarian anti
6	343	72.8	974	22	AAFP9935 Human secreted pro
7	332.4	70.6	973	22	AAFP9903 Human secreted pro
8	291.6	61.9	1173	23	AA81308 DNA encoding novel
9	291	61.8	291	20	AA60503 Human persephin pr

10	289.4	61.4	291	20	AA60505	Human persephin pr
11	250	53.1	471	20	AA60497	WO9914235 Seq ID N
12	250	53.1	471	20	AA60489	Murine pro-pro per
13	207.6	44.1	405	18	AAT90762	Mature mouse perse
14	207.6	44.1	405	20	AA60485	WO9914235 Seq ID N
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17	207.6	44.1	559	20	AA60471	WO9914235 Seq ID N
18	207.6	44.1	594	21	AAZ50344	Murine persephin ge
19	207.6	44.1	723	20	AA60487	WO9914235 Seq ID N
20	203	43.1	559	18	AAT90805	Rat persephin gene
21	203	43.1	559	20	AA60495	WO9914235 Seq ID N
22	203	43.1	559	21	AAZ50345	Rat Persephin gene
23	201.4	42.8	559	20	AA60472	WO9914235 Seq ID N
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27	195	41.4	291	18	AAT90763	Mature mouse perse
28	195	41.4	291	20	AA60501	Rat persephin cdna
29	195	41.4	291	20	AA60486	WO9914235 Seq ID N
30	189.6	40.3	391	20	AA60460	WO9914235 Seq ID N
31	186.6	39.6	273	20	AA60451	WO9914235 Seq ID N
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41	148.8	31.6	336	20	AA60459	WO9914235 Seq ID N
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44	79.8	16.9	306	18	AAT61468	Mature human neut
45	79.8	16.9	306	20	AA60401	WO9914235 Seq ID N

ALIGNMENTS

RESULT 1

AA60507
ID AAX60507 standard; cdna; 471 BP.

XX AAX60507;

AC AAX60507;

XX 17-AUG-1999 (first entry)

DT Human pre-pro persephin cdna sequence.

DE Human pre-pro persephin cdna sequence.

XX Growth factor; GF; persephin; neuron growth; cellular degeneration;

KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;

KW brain injury; spinal cord injury; nervous system tumour; infection;

KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;

KW metabolic disease; diabetes; renal dysfunction; neurturin; ss.

XX Homo sapiens.

XX WO9914235-A1.

XX 25-MAR-1999.

XX 15-SEP-1998; 98WO-US19163.

XX 16-SEP-1997; 97US-0931858.

XX (UNIW) UNIV WASHINGTON.

XX Desauvage F, Johnson EM, Klein R, Kotzbauer PT;

PI Lampe PA, Milbrandt JD;

PS Claim 15; Page 198; 222pp; English.
 XX The invention relates to a novel isolated and purified growth factor (GF)
 CC that comprises persephin or a fragment or a conservatively substituted
 CC variant. The persephin GF polypeptides can promote the survival and
 CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
 CC or polynucleotides can be used for preventing or treating cellular
 CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
 CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,
 CC acute brain injury, acute spinal cord injury, nervous system tumours,
 CC multiple sclerosis, or infection, hematopoietic cell degeneration or
 CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or
 CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
 CC resulting from cardiomyopathy or congestive heart failure. They can also
 CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
 CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions
 CC and damage caused by infectious agents. The GF can also be used for
 CC promoting the growth and/or differentiation of a cell in a culture
 CC medium. The antisense polynucleotides can be used for treating a disease
 CC condition mediated by expression of persephin by a population of cells.
 CC The products can also be used for detection and diagnosis.
 XX
 SQ Sequence 291 BP; 33 A; 111 C; 99 G; 48 T; 0 other;
 Query Match 61.8%; Score 291; DB 20; Length 291;
 Best Local Similarity 100.0%; Pred. No. 4.8e-50;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 181 GCCCTGCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGCGTGCGCAGAGCTAGGCCCTG 240
 DB 1 GCCCTGCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGCGTGCGCAGAGCTAGGCCCTG 60
 QY 241 GCGTACGCTCAGAGAGAGGTCTCTCCGCTACTGCGCGGCGAGCTGCCCCCGTGGT 300
 DB 61 GCGTACGCTCAGAGAGAGGTCTCTCCGCTACTGCGCGGCGAGCTGCCCCCGTGGT 120
 QY 301 GCCCGCACCAGCATGGCTGGCGCTGGCGGCTCAGGGCAGGGCGGCCAGCCACGCT 360
 DB 121 GCCCGCACCAGCATGGCTGGCGCTGGCGGCTCAGGGCAGGGCGGCCAGCCACGCT 180
 QY 361 GGSCCTGCTGCGCGGCCACTCGCTACACCGAGTGGCCCTTCTCGATGACCGCCACCGC 420
 DB 181 GGSCCTGCTGCGCGGCCACTCGCTACACCGAGTGGCCCTTCTCGATGACCGCCACCGC 240
 QY 421 TGGCAGGGCTGCCCCAGCTCTCGCGGCTGCGCTGCGGCTGTGGTGGCTGA 471
 DB 241 TGGCAGGGCTGCCCCAGCTCTCGCGGCTGCGCTGCGGCTGTGGTGGCTGA 291

RESULT 10
 AAX60505
 ID AAX60505 standard; cDNA: 291 BP.
 XX
 AC AAX60505;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE Human persephin protein encoding cDNA.
 XX
 KW Growth factor; GF; persephin; neuron growth; cellular degeneration;
 KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
 KW brain injury; spinal cord injury; nervous system tumour; infection;
 KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;
 KW metabolic disease; diabetes; renal dysfunction; neurturin; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9914235-A1.
 XX
 PD 25-MAR-1999.
 XX

PF 15-SEP-1998; 98WO-US19163.
 XX
 PR 16-SEP-1997; 97US-0931858.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Desauvage F, Johnson EM, Klein R, Kotzbauer PT,
 PI Lampe PA, Milbrandt JD;
 XX
 XX WPI: 1999-244023/20.
 DR
 XX New isolated persephin growth factor nucleic acids used to, e.g.
 PT promote neuronal growth
 PT
 XX Claim 15; Page 199; 222pp; English.
 XX
 CC The invention relates to a novel isolated and purified growth factor (GF)
 CC that comprises persephin or a fragment or a conservatively substituted
 CC variant. The persephin GF polypeptides can promote the survival and
 CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
 CC or polynucleotides can be used for preventing or treating cellular
 CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
 CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,
 CC acute brain injury, acute spinal cord injury, nervous system tumours,
 CC multiple sclerosis, or infection, hematopoietic cell degeneration or
 CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or
 CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
 CC resulting from cardiomyopathy or congestive heart failure. They can also
 CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
 CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions
 CC and damage caused by infectious agents. The GF can also be used for
 CC promoting the growth and/or differentiation of a cell in a culture
 CC medium. The antisense polynucleotides can be used for treating a disease
 CC condition mediated by expression of persephin by a population of cells.
 CC The products can also be used for detection and diagnosis.
 XX
 SQ Sequence 291 BP; 33 A; 112 C; 99 G; 47 T; 0 other;
 Query Match 61.4%; Score 289.4; DB 20; Length 291;
 Best Local Similarity 99.7%; Pred. No. 1e-49;
 Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 181 GCCCTGCTGTGTCATGCCAGCTGTGGAGCCTGACCCCTGTCGTCGCGCAGAGCTAGGCCCTG 240
 DB 1 GCCCTGCTGTGTCATGCCAGCTGTGGAGCCTGACCCCTGTCGTCGCGCAGAGCTAGGCCCTG 60
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 DB 61 GGCTAGGCTCAGAGAGAGGTCTCTCCGCTACTGCGCGGCGAGCTGCCCCCGTGGT 120
 QY 301 GCCCGCACCAGCATGGCTGGCGCTGGCGGCTGCGAGGCGAGGGCGGCCAGCCACGCT 360
 DB 121 GCCCGCACCAGCATGGCTGGCGCTGGCGGCTGCGAGGCGAGGGCGGCCAGCCACGCT 180
 QY 361 GGCGCCCTGCTGCGCGGCCACTCGCTACACCGAGTGGCCCTTCTCGATGACCGCCACCGC 420
 DB 181 GGCGCCCTGCTGCGCGGCCACTCGCTACACCGAGTGGCCCTTCTCGATGACCGCCACCGC 240
 QY 421 TGGCAGGGCTGCCCCAGCTCTCGCGGCTGCGCTGCGGCTGTGGTGGCTGA 471
 DB 241 TGGCAGGGCTGCCCCAGCTCTCGCGGCTGCGCTGCGGCTGTGGTGGCTGA 291
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 ID AAX60497 standard; cDNA: 471 BP.
 XX
 AC AAX60497;
 XX
 DT 17-AUG-1999 (first entry)
 XX
 DE WO9914235 Seq ID No: 190.

Qy 162 CTTGCCGCGCTGCGCCAGCCCTGTCTGTCCATGCCAGCTGTGGAGCCTGACCCCTGTC 221
Db 120 CCATGTCGCTCTTCCAAGAGCCTTGGCTGGTTCATGCCGACTGTGGAGCCTGACCCCTACC 179
Qy 222 CGTGGCAGAGCTAGGCCCTGGGCTACGCCCTCAGAGGAGAAAGTCACTTTCGCCCTACTGCGC 281
Db 180 AGTGGCTCAGCTGGGCTGGGCTATGCCCTCGGAGGAGAAAGTCACTTTCGGATACTGTGC 239
Qy 282 CGGCAGCTGCCCGCGCTGTGTGGCCGACCCAGCATGGCCCTGGCGCTGGCCCGGCTCCAGGG 341
Db 240 TGGCAGCTGTCCCAAGAGGCGCGTACCCAGCAGTCTGGTACTGGCCCGGCTTCGAGG 299
Qy 342 CCAGGGCGAGCCACGGTGGGCGCTGTGCGGCGCCACTCGCTACACCCGACGCTGGCCCTT 401
Db 300 GCGGGTCGAGCCCATGGCCGACCCCTGTGCCAGCCACAGCTATGCTGATGTGACCTT 359
Qy 402 CCTCGATACGCCCAACCGCTGGCAGCGGCTGGCCGAGCTCTCGGGGGGCTGCCCTGGGGCTG 461
Db 360 CTTGATGATCAGCACCATTTGGCAGCAGCTGCCTCAGCTCTCAGCTGCAGCTTGTGGCTG 419
Qy 462 TGGTGGCTGA 471
Db 420 TGGTGGCTGA 429

Search completed: March 7, 2003, 11:44:13
Job time : 316 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:36:19 ; Search time 2458 Seconds
(without alignments)
3103.366 Million cell updates/sec

Title: US-09-220-617B-203
Perfect score: 471
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:**
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2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	83.2	17.7	518	10	AW050617
C 3	79.8	16.9	643	13	BM665236
C 4	79.8	16.9	722	14	BM677930
5	79.8	16.9	753	14	BQ189286
6	78.8	16.7	839	17	CNS01VCA

7	69.2	14.7	1544	11	AK015393	Mus muscu
8	68.4	14.5	1025	17	CNS0223X	Tetraodon
9	67.2	14.3	439	10	AW611702	AW611702 hg86d07.x
10	66.4	14.1	670	10	BB641881	BB641881 wh22g09.x
11	66.2	14.1	514	9	AI768514	AI768514 wh22g09.x
12	63.4	13.5	925	17	CNS0091P	AL053013 Drosophi
13	62.8	13.3	932	17	CNS0072Q	AL066742 Drosophi
14	62.4	13.2	932	17	CNS0072Q	AL066742 Drosophi
15	61.8	13.1	604	14	BM725812	BM725812 UI-E-EJ0-
16	61.6	13.1	600	14	BM726983	BM726983 UI-E-EJ0-
17	61	13.0	1080	17	CNS04PM4	AL301477 Tetraodon
18	60.8	12.9	522	12	BF416337	BF416337 UI-R-CAO-
19	60.4	12.8	471	12	BF416337	BF416337 UI-R-CAO-
20	60.4	12.8	489	12	BF407806	BF407806 UI-R-CUO-
21	60	12.7	464	14	BM899804	BM899804 UI-R-BJ2-
22	60	12.7	546	14	BQ209765	BQ209765 UI-R-DZ1-
23	59.6	12.7	925	17	CNS0091P	AL053013 Drosophi
24	58	12.3	839	17	CNS004NB	AL054280 Drosophi
25	57.8	12.3	670	10	BB547879	BB547879 BB547879
26	57.4	12.2	693	14	BQ192656	BQ192656 UI-R-DL1-
27	57.2	12.1	679	14	BM702521	BM702521 UI-E-CL1-
28	57.2	12.1	1203	17	CNS015Y4	AL106054 Drosophi
29	54.8	11.6	350	9	AI598581	AI598581 EST250270
30	54.6	11.6	365	9	AI548543	AI548543 UI-R-C3-t
31	54.6	11.6	1160	11	AK002508	AK002508 Mus muscu
32	54.2	11.5	854	13	BI407479	BI407479 602919290
33	53.6	11.4	1538	17	AG030607	AG030607 Pan trogl
34	53.2	11.3	813	17	A2193936	A2193936 SP_1025_A
35	53.2	11.3	938	17	AG130978	AG130978 Pan trogl
36	52.4	11.1	935	17	CNS006XK	AL066051 Drosophi
37	52.4	11.1	935	17	CNS006XK	AL066051 Drosophi
38	52.4	11.1	1101	17	CNS017SY	AL108460 Drosophi
39	52.2	11.1	776	17	CNS010RY	AL099352 Drosophi
40	51.6	11.0	1009	17	CNS010EW	AL099352 Drosophi
41	51.4	10.9	704	17	AG060135	AG060135 Pan trogl
42	51.4	10.9	960	17	AG036217	AG036217 Pan trogl
43	51.4	10.9	1128	14	BQ710735	BQ710735 AGENCOURT
44	51.2	10.9	1040	12	BG786331	BG786331 SEAMC006
45	51.2	10.9	1244	12	BG846745	BG846745 1024014H0

ALIGNMENTS

RESULT 1
BM987233/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM987233
UI-H-CO0-aql-e-08-0-UI.s1 NCICGAP_Sub9 Homo sapiens CDNA clone
IMAGE: 3104342.3', mRNA sequence.
BM987233.1 GI:19706622
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 510)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. 510

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:33:49 ; Search time 2567 Seconds
(without alignments)
5339.860 Million cell updates/sec

Title: US-09-220-617B-203
Perfect score: 471
Sequence: 1 ATGGCGTAGGGAAGTTCTCT.....CCTGGCGCTGGTGGCTCA 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_ov.*
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- 11: gb_sts.*
- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_md.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
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- 27: em_sts.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sv.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	471	100.0	471	9	AF040962 Homo sapi
2	372.8	79.2	2180	9	AK055490 Homo sapi
3	372.8	79.2	118819	9	AC011491 Homo sapi
4	250	53.1	471	10	AF040960
5	250	53.1	471	10	AF040961
6	207.6	44.1	405	6	AF040961 Rattus no
7	207.6	44.1	544	6	AR152134 Sequence
8	207.6	44.1	559	6	AR152107 Sequence
9	206	43.7	213137	10	AC073683
10	203	43.1	559	6	AR152121 Sequence
11	203	43.1	142758	2	AC129629 Rattus no
12	199.8	42.4	291	6	AR152133 Sequence
13	195	41.4	291	6	AR152135 Sequence
14	189.6	40.3	391	6	AR152109 Sequence
15	186.6	39.6	273	6	AR152100 Sequence
16	180.6	38.3	267	6	AR152098 Sequence
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18	148.8	31.6	336	6	AR152104 Sequence
19	148.8	31.6	336	6	AR152108 Sequence
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21	79.8	16.9	306	6	AR005328 Sequence
22	79.8	16.9	306	6	AR044780 Sequence
23	79.8	16.9	306	6	AR062886 Sequence
24	79.8	16.9	306	6	AR152050 Sequence
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33	79.8	16.9	591	6	AR062988 Sequence
34	79.8	16.9	591	6	AR152052 Sequence
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36	79.8	16.9	1160	9	HSU802618
37	79.8	16.9	80893	9	AC024592
38	79.8	16.9	187488	2	AC010454
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40	69.2	14.7	675	6	AX470388
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ALIGNMENTS

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ACCESSION AF040962
VERSION AF040962.1
KEYWORDS GI:2935709
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
REFERENCE
AUTHORS Milbrandt, J., de Sauvage, F. J., Fahrner, T. J., Baloh, R. H.,
Leitner, M. L., Tansey, M. G., Lampe, P. A., Heuckeroth, R. O.,
Kotzbauer, P. T., Simburger, K. S., Golden, J. P., Davies, J. A.,

AF040962 471 bp mRNA linear PRI 06-MAR-1998

3

Unclassified.					
REFERENCE	1	(bases 1 to 405)			
AUTHORS	Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.				
TITLE	Persperhin and related growth factors				
JOURNAL	Patent: US 6232449-A 175 15-MAY-2001;				
FEATURES	Location/Qualifiers				
source	1..405				
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ORIGIN	/organism="unknown"				
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Best Local Similarity	79.4%;	Pred. No. 3.8e-26;			
Matches 246;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;	
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QY	222	CGTGGCAGACTAGGCCTGGGCTAGCGCTCAGAGGAGAAGTCACTCTCCGCTACTCGGC	281		
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QY	282	CGCAGCTGCCCGCTGGTGGCCGACCCACAGCATGGCTGGCGCTGGCCCGCTGCAGGG	341		
Db	216	TGGCAGCTGTCCCAGAGGCCCTACCCACACAGTCTGGTACTGGCCCCGGCTCGAGG	275		
QY	342	CCAGGGCGAGCCACCGTGGGCGCTGTGTCGGCGCCCACTCGCTACACCGACGTGGCCTT	401		
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QY	402	CCTCGATACCGCCACCGCTGGCAGGGCTGCCCCAGCTCTCGCGGGCTGCTCGGGCTG	461		
Db	336	CCTTGATGATCAGCACCATGGCAGCAGCTGCCTCAGCTCTCAGCTGCAGCTTGTGGCTG	395		
QY	462	TGGTGGCTGA 471			
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LOCUS	AR152107	544 bp	DNA	Linear	PAT 08-AUG-2001
DEFINITION	Sequence 105 from patent US 6232449.				
ACCESSION	AR152107				
VERSION	AR152107.1	GI:15118157			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
Unclassified.					
REFERENCE	1	(bases 1 to 544)			
AUTHORS	Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.				
TITLE	Persperhin and related growth factors				
JOURNAL	Patent: US 6232449-A 105 15-MAY-2001;				
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source	1..544				
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Query Match	44.1%	Score 207.6;	DB 6;	Length 544;	
Best Local Similarity	79.4%;	Pred. No. 3.5e-26;			
Matches 246;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;	
QY	162	CCTTGCCCGCTGCGCCGAGCCCTGTCTGGTCCATGCCAGCTGTGGAGCCTGACCCCTGTC	221		
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QY	222	CGTGGCAGACTAGGCCTGGGCTACGCTCAGAGGAGAAGTCACTCTCCGCTACTCGGC	281		
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 213137)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Unpublished
REFERENCE 2 (bases 1 to 213137)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 213137)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Submitted (26-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 5 (bases 1 to 213137)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Submitted (05-APR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
REFERENCE 6 (bases 1 to 213137)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Submitted (16-APR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 5, 2002 this sequence version replaced gi:18767417.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 1.2.
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source
1..213137
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/db_xref="taxon:10090"
/chromosome="17"
/clone="RP23-124G7"
BASE COUNT 52043 a 52563 c 52259 g 56272 t
ORIGIN

Query Match 43.7%; Score 206; DB 10; Length 213137;
Best Local Similarity 79.0%; Pred. No. 1.7e-26;
Matches 245; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 162 CTTGCGCCGCTGCGCCGAGCGCTGTCTGGTCCATGCCAGCTGTGGAGCCTGACCTGTGC 221
DB 8066 CCATGTCCTCTTCCAAAGAGCGCTTGGCTGTCTATGCCGACTGTGGAGCCTGACCCCTAC 8125
QY 222 CTGGCAGAGTAGGCTGCGGTACCCCTCAGAGGAGAGGTACATCTCCGCTACTGCGCG 281
DB 8126 AGTGGCTGAGCTGGGCGCTGGGCTATGCCCTCGGAGGAGAGGTATCTCCGATATGTGC 8185
QY 282 CGGACGCTGCCCGCTGGTGGCCGACCCAGCATGGCCCTGGGCGTGGCCGCTGCGAGG 341
DB 8186 TGGCAGCTGTCCCAAGAGGCCATACCCAGCACAGTCTGGTACTTGGCCGCGCTTCGAGG 8245
QY 342 CCAGGCCGAGCCGCTGGGCGCTGTCTGGCGGCCACTCGCTACACCGAGCTGGCCCTT 401
DB 8246 GCGGGGTGAGGCCCATGGCGACCCCTGTCTGCCAGCCACAGCTATGTGATGTGACCTT 8305
QY 402 CTTGATACCGCCACCGCTGGCAGCGGCTGCCCGAGCTCTCGGCGGCTGCGCTGCGGCTG 461
DB 8306 CCTTGATGATCAGCACCATTTGGCAGGAGCTGCTCAGCTCCTCAGCTGACGCTTGGGCTG 8365
QY 462 TGGTGGCTGA 471

Db 8366 TGGTGGCTGA 8375
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RESULT 10
LOCUS AR152121
DEFINITION Sequence 134 from patent US 6232449.
ACCESSION AR152121
VERSION AR152121.1 GI:15118171
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 559)
AUTHORS Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6232449-A 134 15-MAY-2001;
FEATURES Location/Qualifiers
source
1..559
/organism="unknown"
BASE COUNT 104 a 166 c 150 g 139 t
ORIGIN
Query Match 43.1%; Score 203; DB 6; Length 559;
Best Local Similarity 78.8%; Pred. No. 2.1e-25;
Matches 242; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 165 TGCCTGCTGCGCCGAGCGCTGTCTGGTCCATGCCAGCTGTGGAGCCTGACCTGTCCGT 224
DB 253 TGTCCGCTTCCCAAGAGCGCTTACCTGGTTGTGCGCGCTGTGGAGCCTGACCTACCACT 312
QY 225 GGCAGAGCTAGGCTGGGCTAGCGCTCAGAGGAGAGGTATCTTCCGCTACTGCGCGG 284
DB 313 GCTGAGCTTGGCTGGGCTATGCCCTCAGAGGAGAGGATATCTTCCGATATGTGCTGG 372
QY 285 CAGCTGCCCGCTGGTGGCCGACCCAGCATGGCTGGCGCTGGCCGCGCTGCAGGGGCA 344
DB 373 CAGCTGTCCCAAGAGGTCCGTACCCAGCACAGTCTGGTGTCTGGCGCGCTTTCGAGGGCA 432
QY 345 GGGCGGCGCCAGCGTGGGCGCTGCTGCGCGCCACTCGCTACACCGAGCTGGCCTTCT 404
DB 433 GGGTGCAGCTCATGGCAGACCTTGTGCGAGCCACCACTATGTGATGTGACCTTCTCT 492
QY 405 CGATGACCGCCACCGCTGGCAGCGCTGCCCGAGCTCTCGGCGGCTGCTGCGGCTGTGG 464
DB 493 TGATGACCAACCATTTGGCAGCAGCTGCCTCAGCTCCTCAGCGGAGCTTGTGGCTGTGG 552
QY 465 TGGCTGA 471
|||||||
Db 553 TGGCTGA 559
AC129629 142758 bp DNA linear HTG 24-AUG-2002
Rattus norvegicus clone CH230-117J15, *** SEQUENCING IN PROGRESS
DEFINITION *** 74 unordered pieces.
ACCESSION AC129629.1 GI:22024375
VERSION HTG: HTGS_PHASE1.
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 142758)
AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Gant, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, N., Hernandez, J., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Manqum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarunpugon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, R., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajd, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Syatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tindley, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 142758)
Worley, K.C.

Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 142758)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYO
Center clone name: CH230-117J15
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 63896 bases at least Q40
Consensus quality: 69524 bases at least Q30
Consensus quality: 73620 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1051: contig of 1051 bp in length
1052 1151: gap of unknown length
1152 2432: contig of 1271 bp in length
2423 2522: gap of unknown length
2523 3785: contig of 1243 bp in length
3786 3865: gap of unknown length
3866 4877: contig of 1011 bp in length
4877 6421: gap of unknown length
6421 6521: contig of 1445 bp in length
6521 6522: gap of unknown length
6522 7566: contig of 1045 bp in length
7566 7667: gap of unknown length
7667 8814: contig of 1048 bp in length
8814 9932: contig of 1178 bp in length
9932 10092: gap of unknown length
10092 11721: contig of 1629 bp in length
11721 11821: gap of unknown length
11821 12916: contig of 1095 bp in length
12916 13016: gap of unknown length
13016 14068: contig of 1052 bp in length
14068 14168: gap of unknown length
14168 15291: contig of 1123 bp in length
15291 15391: gap of unknown length
15391 16334: contig of 1143 bp in length
16334 16634: gap of unknown length
16634 17883: contig of 1249 bp in length
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17983 19034: contig of 1071 bp in length
19034 19154: gap of unknown length
19154 20588: contig of 1434 bp in length
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20688 21775: contig of 1087 bp in length
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25315 26364: contig of 1049 bp in length
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27555 27656: gap of unknown length
27656 29417: contig of 1662 bp in length
29417 29517: gap of unknown length
29517 31140: contig of 1623 bp in length
31140 31240: gap of unknown length
31240 32270: contig of 1030 bp in length
32270 32370: gap of unknown length
32370 34165: contig of 1795 bp in length
34165 34265: gap of unknown length
34265 35438: contig of 1173 bp in length
35438 35538: gap of unknown length
35538 36965: contig of 1427 bp in length
36965 37065: gap of unknown length
37065 38188: contig of 1123 bp in length
38188 38288: gap of unknown length
38288 39399: contig of 1111 bp in length
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41093 41193: gap of unknown length
41193 42376: contig of 1183 bp in length
42376 42476: gap of unknown length
42476 42377


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Db 181 AGACCTTGCCTGCAGCCACCACTATGCTGATGTGACCTTCTTGTATGACCAACCAT 240
QY 421 TGGCAGCGGTGCGCCAGCTCTCGGGCGCTGCGCTGCGGCTGTGGTGGCTGA 471
Db 241 TGGCAGCAGCTGCTCAGCTCTCAGCGCAGCTTGTGGCTGTGGTGGCTGA 291

RESULT 14
LOCUS AR152109 391 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 107 from patent US 6232449.
ACCESSION AR152109
VERSION AR152109.1 GI:15118159
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 391)
AUTHORS Johnson,E.M. Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6232449-A 107 15-MAY-2001;
FEATURES
    Location/Qualifiers
    source 1..391
    /organism="unknown"

BASE COUNT 84 a 106 c 117 g 84 t
ORIGIN

Query Match 40.3%; Score 189.6; DB 6; Length 391;
Best Local Similarity 80.4%; Pred. No. 4.6e-23;
Matches 222; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 196 TGCACGCTGGAGCCTGACCCCTGTCGGTGGCAGAGCTAGGCCCTGGGCTACGCTCAGAG 255
Db 1 TGCCTGGCTGGAGCCTGACCCCTGTCGGTGGCAGAGCTAGGCCCTGGGCTATGCTCAGAG 60

QY 256 GAGAAGTATCTTCGGCTACTCGCGCGCAGCTGCCCGCTGGTGGCCCGCACCCAGCAT 315
Db 61 GAGAAGTATCTTCGGCTACTGTCGGTGGCAGAGCTAGGCCCTGGGCTATGCTCAGAG 120

QY 316 GGCTGGCGCTGCGCCGGCTGTCAGGGCCAGGGCCAGCCACCGTGGGCGCTGCTGCCGG 375
Db 121 AGTCTGGTGTGCGCGCTCTTCGAGGGCAGGGTTCGAGCTCATGGCAGACCTTGCCTGCAG 180

QY 376 CCCACTCGCTACACCGACGCTGGCCTTCCTCGATGACCGCCACCGCTGGCAGCGCTGCC 435
Db 181 CCCACGAGCTATGCTGATGACCTTCTTGTATGACCAACCATTTGGCAGCAGCTGCCT 240

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ORIGIN

Query Match 39.6%; Score 186.6; DB 6; Length 273;
Best Local Similarity 80.2%; Pred. No. 1.6e-22;
Matches 219; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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QY 256 GAGAAGTATCTTCGGCTACTCGCGCGCAGCTGCCCGCTGGTGGCCCGCACCCAGCAT 315
Db 61 GAGAAGTATCTTCGGCTACTGTCGGTGGCAGAGCTAGGCCCTGGGCTATGCTCAGAG 120

QY 316 GGCTGGCGCTGCGCCGGCTGTCAGGGCCAGGGCCAGCCACCGTGGGCGCTGCTGCCGG 375
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